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Reviewer: markspencer

Timestamp: [year=2008; month=12; day=16; hr=15; min=39; sec=26; ms=904;
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Application No: 10593567

Version No: 1.0

Input Set:

Output Set:

Started: 2008-12-01 16:03:08.543

Finished: 2008-12-01 16:03:09.613

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 70 ms

Total Warnings: 9

Total Errors: 0

No. of SeqIDs Defined: 13

Actual SeqID Count: 13

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)

SEQUENCE LISTING

<110> GROGER, HARALD
 WERNER, HELGE
 ALTENBUCHNER, JOSEF
 MENZEL, ANNE
 HUMMEL, WERNER

<120> PROCESS FOR PREPARING OPTICALLY ACTIVE AMINO ACIDS USING A
 WHOLE-CELL CATALYST

<130> 294227US-10757-9350-0-X PCT

<140> 10593567

<141> 2008-12-01

<150> PCT/EP2005/002933

<151> 2005-03-18

<150> DE 102004014280.7

<151> 2004-03-22

<160> 13

<170> PatentIn version 3.5

<210> 1

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 1

aaaaaactta agaaggagat atacatatga cattagaaat cttcgaa

47

<210> 2

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 2

aaaaaactgc agttagcgac ggctaataat at

32

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 3
aaaaaacata tgaagattgt cttagttctt 30

<210> 4
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 4
aaaaaagacg tcttatttct tatcgtgttt acc 33

<210> 5
<211> 1120
<212> DNA
<213> Bacillus cereus

<220>

<221> CDS
<222> (20)..(1120)

<400> 5
ttaagaagga gatatacat atg aca tta gaa atc ttc gaa tac tta gaa aaa 52
Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys
1 5 10

tat gat tat gag caa gta gta ttt tgt caa gat aaa gaa tct ggt tta 100
Tyr Asp Tyr Glu Gln Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu
15 20 25

aaa gca att att gca att cat gat aca aca ctt gga ccg gct ctt ggt 148
Lys Ala Ile Ile Ala Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly
30 35 40

gga aca aga atg tgg aca tat gat tct gaa gaa gcg gcg att gaa gat 196
Gly Thr Arg Met Trp Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp
45 50 55

gca ttg cgt ctt gca aaa ggg atg aca tac aaa aac gca gca gct ggt 244
Ala Leu Arg Leu Ala Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly
60 65 70 75

tta aac tta ggt ggt gcg aaa aca gta att atc ggt gat cct cgt aaa 292
Leu Asn Leu Gly Gly Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys
80 85 90

gat aag agc gaa gca atg ttc cgt gca cta gga cgt tat atc caa gga	340
Asp Lys Ser Glu Ala Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly	
95 100 105	
cta aac gga cgt tac att aca gct gaa gat gtt ggt aca aca gta gat	388
Leu Asn Gly Arg Tyr Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp	
110 115 120	
gat atg gat att atc cat gaa gaa act gac ttt gta aca ggt atc tca	436
Asp Met Asp Ile Ile His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser	
125 130 135	
cca tca ttc ggt tct tct ggt aac cca tct ccg gta act gca tac ggt	484
Pro Ser Phe Gly Ser Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly	
140 145 150 155	
gtt tac cgt ggt atg aaa gca gct gca aaa gaa gct ttc ggt act gac	532
Val Tyr Arg Gly Met Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp	
160 165 170	
aat tta gaa gga aaa gta att gct gtt caa ggc gtt ggt aac gta gca	580
Asn Leu Glu Gly Lys Val Ile Ala Val Gln Gly Val Gly Asn Val Ala	
175 180 185	
tat cac cta tgc aaa cat tta cac gct gaa gga gca aaa tta att gtt	628
Tyr His Leu Cys Lys His Leu His Ala Glu Gly Ala Lys Leu Ile Val	
190 195 200	
aca gat att aat aaa gaa gct gta caa cgt gct gta gaa gaa ttc ggt	676
Thr Asp Ile Asn Lys Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly	
205 210 215	
gca tca gca gtt gaa cca aat gaa att tac ggt gtt gaa tgc gat att	724
Ala Ser Ala Val Glu Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile	
220 225 230 235	
tac gca cca tgt gca cta ggc gca aca gtt aat gat gaa act att cca	772
Tyr Ala Pro Cys Ala Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro	
240 245 250	
caa ctt aaa gca aaa gta atc gca ggt tct gcg aat aac caa tta aaa	820
Gln Leu Lys Ala Lys Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys	
255 260 265	
gaa gat cgt cat ggt gac atc att cat gaa atg ggt att gta tac gca	868
Glu Asp Arg His Gly Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala	
270 275 280	
cca gat tat gta att aat gca ggt ggc gta att aac gta gca gac gaa	916
Pro Asp Tyr Val Ile Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu	
285 290 295	
tta tat gga tac aat aga gaa cgt gca cta aaa cgt gtt gag tct att	964
Leu Tyr Gly Tyr Asn Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile	
300 305 310 315	
tat gac acg att gca aaa gta atc gaa att tca aaa cgc gat ggc ata	1012

Tyr Asp Thr Ile Ala Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile
320 325 330

gca act tat gta gcg gca gat cgt cta gct gaa gag cgc att gca agc 1060
Ala Thr Tyr Val Ala Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser
335 340 345

ttg aag aat tct cgt agc act tac tta cgc aac ggt cac gat att att 1108
Leu Lys Asn Ser Arg Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile
350 355 360

agc cgt cgc taa 1120
Ser Arg Arg
365

<210> 6

<211> 366

<212> PRT

<213> Bacillus cereus

<400> 6

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met			
145	150	155	160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys			
165	170	175	
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys			
180	185	190	
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys			
195	200	205	
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu			
210	215	220	
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala			
225	230	235	240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys			
245	250	255	
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly			
260	265	270	
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile			
275	280	285	
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn			
290	295	300	
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala			
305	310	315	320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala			
325	330	335	
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg			
340	345	350	
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg			
355	360	365	

<210> 7
<211> 1095
<212> DNA
<213> Candida boidinii

<220>
<221> CDS
<222> (1)..(1095)

<400> 7
atg aag att gtc tta gtt ctt tat gat gct ggt aag cac gct gct gat 48
Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp
1 5 10 15

gaa gaa aaa tta tat ggt tct act gaa aat aaa tta ggt att gct aat 96
Glu Glu Lys Leu Tyr Gly Ser Thr Glu Asn Lys Leu Gly Ile Ala Asn
20 25 30

tgg tta aaa gat caa ggt cat gaa cta att act act tct gat aaa gaa 144
Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
35 40 45

ggt gaa aca agt gaa ttg gat aaa cat atc cca gat gct gat att atc 192
Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile
50 55 60

atc acc act cct ttc cat cct gct tat atc act aag gaa aga ctt gac 240
Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp
65 70 75 80

aag gct aag aac tta aaa tta gtc gtt gtc gct ggt gtt ggt tct gat 288
Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
85 90 95

cac att gat tta gat tat att aat caa aca ggt aag aaa atc tca gtc 336
His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
100 105 110

ctg gaa gtt aca ggt tct aat gtt gtc tct gtt gct gaa cac gtt gtc 384
Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
115 120 125

atg acc atg ctt gtc ttg gtt aga aat ttc gtt cca gca cat gaa caa 432
Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
130 135 140

att att aac cac gat tgg gag gtt gct gct atc gct aag gat gct tac 480
Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
145 150 155 160

gat atc gaa ggt aaa act atc gct acc att ggt gct ggt aga att ggt 528
Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
165 170 175

tac aga gtc ttg gaa aga tta ctc cca ttt aat cca aaa gaa tta tta 576
Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu

180	185	190	
tac tac gat tat caa gct tta cca aaa gaa gct gaa gaa aaa gtt ggt			624
Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly			
195	200	205	
gct aga aga gtt gaa aat att gaa gaa tta gtt gct caa gct gat atc			672
Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile			
210	215	220	
gtt aca gtt aat gct cca tta cac gca ggt aca aaa ggt tta att aat			720
Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn			
225	230	235	240
aag gaa tta tta tct aaa ttt aaa aaa ggt gct tgg tta gtc aat acc			768
Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr			
245	250	255	
gca aga ggt gct att gct gtt gct gaa gat gtt gca gca gct tta gaa			816
Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu			
260	265	270	
tct ggt caa tta aga ggt tac ggt ggt gat gtt tgg ttc cca caa cca			864
Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro			
275	280	285	
gct cca aag gat cac cca tgg aga gat atg aga aat aaa tat ggt gct			912
Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala			
290	295	300	
ggg aat gcc atg act cct cac tac tct ggt act act tta gac gct caa			960
Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln			
305	310	315	320
aca aga tac gct gaa ggt act aaa aat att ttg gaa tca ttc ttt acc			1008
Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr			
325	330	335	
ggg aaa ttt gat tac aga cca caa gat att atc tta tta aat ggt gaa			1056
Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu			
340	345	350	
tac gtt act aaa gct tac ggt aaa cac gat aag aaa taa			1095
Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys			
355	360		

<210> 8

<211> 364

<212> PRT

<213> Candida boidinii

<400> 8

Met	Lys	Ile	Val	Leu	Val	Leu	Tyr	Asp	Ala	Gly	Lys	His	Ala	Ala	Asp
1			5						10						15

Glu Glu Lys Leu Tyr Gly Ser Thr Glu Asn Lys Leu Gly Ile Ala Asn
20 25 30

Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
35 40 45

Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile
50 55 60

Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp
65 70 75 80

Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
85 90 95

His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
100 105 110

Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
115 120 125

Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
130 135 140

Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
145 150 155 160

Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
165 170 175

Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu
180 185 190

Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly
195 200 205

Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile
210 215 220

Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn
225 230 235 240

Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr

245

250

255

Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu
260 265 270

Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
275 280 285

Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
290